



## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<p>(51) International Patent Classification <sup>6</sup> : C12N 15/12, 15/62, 15/55, 15/85, 9/16, 9/64, 5/10, C12Q 1/42, A61K 31/12, 31/275</p>	<p>A2</p>	<p>(11) International Publication Number: <b>WO 98/13488</b>  (43) International Publication Date: 2 April 1998 (02.04.98)</p>
<p>(21) International Application Number: PCT/EP97/05149 (22) International Filing Date: 22 September 1997 (22.09.97) (30) Priority Data: 196 41 180.7 24 September 1996 (24.09.96) DE  (71) Applicant (for all designated States except US): SCHERING AKTIENGESELLSCHAFT [DE/DE]; Patente, Müllerstrasse 178, Postfach 65 03 11, D-13342 Berlin (DE). (72) Inventors; and (75) Inventors/Applicants (for US only): DYRKS, Thomas [DE/DE]; Käthe-Kollwitz-Strasse 25, D-16540 Hohen-Neuendorf (DE). TURNER, Jonathan-David [GB/GB]; 52 Priory Road, West Bridgford, Nottingham NG2 5HU (GB). HARTEL, Marion [DE/DE]; Admiral-Spee-Strasse 1, D-79100 Freiburg (DE).</p>		<p>(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW. ARIPO patent (GH, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).</p> <p><b>Published</b> Without international search report and to be republished upon receipt of that report.</p>
<p>(54) Title: PROCESS FOR THE DETERMINATION OF APP SECRETASE MODULATORS AND THE USE THEREOF AS AGENTS IN THE TREATMENT OF ALZHEIMER'S DISEASE</p>		
<p>(57) Abstract</p> <p>Described are a process for determining the activity of APP secretase using cellular model systems, those cellular systems being used directly for screening for pharmacological modulators of amyloid <math>\beta</math>A4 release, and the modulators that can be identified and isolated by that process as pharmaceutical agents for the treatment of Alzheimer's disease. Also described are expression vectors, cells transfected with the expression vectors and the use thereof in the identification of APP secretase modulators, and a kit for determining APP secretase activity.</p>		

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**Process for the determination of APP secretase modulators and the use thereof  
as agents in the treatment of Alzheimer's disease**

5 The present invention relates to a process for determining the activity of APP secretase using cellular model systems, those cellular systems being used directly for screening for pharmacological modulators of amyloid  $\beta$ A4 release, and to the modulators that can be identified and isolated by that process as pharmaceutical agents for the treatment of Alzheimer's disease.

10 The invention relates also to expression vectors, to cells transfected with the expression vectors and to the use thereof in the identification of APP secretase modulators, and to a kit for determining APP secretase activity.

Alzheimer's disease (AD) is the most frequently occurring dementia disease in the  
15 elderly. 20% of all people aged 80 suffer from this disease. AD is a neuro-degenerative disease having the following characteristic pathological indicators :

1. Intracellular deposits in the form of neurofibrillary tangles (NFTs), chiefly consisting of the Tau protein.
- 20 2. Extracellular amyloid plaques, with the amyloid  $\beta$ A4 peptide as chief component.
3. Amyloid  $\beta$ A4 peptide deposits in the walls of cortical blood vessels.
4. Massive neurone loss in the limbic system and in the cerebral cortex, together with gliosis and atrophy.

25 Amyloid  $\beta$ A4 peptide, which forms the chief component of extracellular deposits, is a peptide 39-43 amino acids long that is released by two proteolytic activities ( $\beta$  and  $\gamma$ -secretases) from a 695-770 amino acid-long transmembrane-bound amyloid precursor protein (APP). Depending on various cell regulation mechanisms, a third  
30 proteolytic activity ( $\alpha$ -secretase) can prevent amyloid  $\beta$ A4 release by enzymatic processing within the amyloid  $\beta$ A4 sequence. In addition to the fact that amyloid  $\beta$ A4 is the chief component of extracellular deposits, it has been possible in a large number of *in vitro* and *in vivo* systems to demonstrate the neurotoxic potential of the peptide and accordingly an experimental correspondence between the formation of  
35 amyloid  $\beta$ A4 and neurodegeneration.

Decisive findings for clarifying the molecular processes involved in AD come from gene technology. Approximately 3% of all AD cases have an autosomal dominant inheritance, the FAD loci having been mapped on chromosome 21, 19, 14 and 1. Three of the FAD genes have been identified and sequenced so far. It has been

possible to demonstrate that mutations in the amyloid precursor protein (APP on chromosome 21) or in the "presenilin" genes (PS1 on chromosome 14 and PS2 on chromosome 1) segregate with the disease. On the basis of those FAD mutations it has been possible to demonstrate conclusively that amyloid  $\beta$ A4 is causatively  
5 involved in the development of the pathological indicators of AD. All mutations found hitherto result in a qualitative or quantitative change in the amyloid  $\beta$ A4 peptide. Modulation (inhibition) of the formation of amyloid  $\beta$ A4 has therefore been one of the main therapeutic approaches.

The simplest modulation of amyloid  $\beta$ A4 formation is effected by a direct or indirect  
10 inhibition or stimulation of the proteases involved in amyloid  $\beta$ A4 release (APP secretases  $\alpha$ ,  $\beta$  or  $\gamma$ ). On the basis of various publications (Kojima S. and Omori M. (1992) FEBS 304, 57-60, McDermott J., Biggins J.A. and Gibson A.M. (1992) BBRC 185, 746-752, Nelson R.B., Siman R., Iqbal M.A. and Potter H. (1993) Journal of Neurochemistry 61, 567-577, Sahasrabudhe S.R., Brown A.M., Hulmes J.D.,  
15 Jacobsen J.S., Vitek M.P., Blume A.J. and Sonnenberg J.L. (1993) Journal of Biological Chemistry 268, 16699-16705, Papastoitsis G., Siman R., Scott R., and Abraham C.R. (1994) Biochemistry 33, 192-199, Matsumoto A. and Fujiwara Y. (1994) Biochemistry 34, 3941-3948, Schönlein C., Löffler J. and Huber G. (1994) BBRC 201, 45-53 and Dreyer R. N., Bausch K. M., Fracasso P., Hammond L. J.,  
20 Wunderlich D., Wirak D. O., Davis G., Brini C. M., Buckholz T. M., König G., Kamarck M. E. and Tamburini P. P. (1994) European Journal of Biochemistry, 224, 265-271) the fact that the APP secretases require a membrane-bound substrate in order to be able to cleave efficiently and specifically must be taken as a starting point.

25 Hitherto described approaches for identifying protease inhibitors that prevent amyloid  $\beta$ A4 release use synthetic peptide substrates to find corresponding protease inhibitors (Sisodia S.S., Koo E.H., Beyreuther K., Unterbeck A. and Price D.L. (1990) Science 248, 492-495 and LeBlanc A.C. and Gambetti P. (1994) BBRC 204, 1371-1380). The cellular activity and specificity of the inhibitors found in that way is, however,  
30 questionable.

It would therefore be desirable to have a process that is suitable for the determination of the activity of APP secretases in intact cells and for the quantitative and differential determination of the APP secretase modulators involved in amyloid  $\beta$ A4 release, and  
35 that, in spite of the complexity of the intact cell system, renders possible a quantitative determination of the proteolytic activity being examined, it being possible for the modulators identifiable and obtainable by the process also to be used as pharmaceutical agents in the treatment of Alzheimer's disease.

A process for the determination of the activity of APP secretase in intact cells and for the identification of modulators of APP secretase activity has now been found which is characterised in that

- 5 a) an expression vector is prepared that comprises a DNA sequence under the control of a promoter, the DNA sequence coding for a fusion polypeptide comprising
  - i) one or more membrane anchor domains,
  - ii) one or more recognition sites for an APP secretase and
  - 10 iii) one or more polypeptide component(s) releasable by cleavage at the recognition site,
- b) the expression vector is introduced into a cell that is capable of expressing one or more APP secretases,
- c) the APP secretase activity in the cells obtained according to step (b) is analysed based on the release of the polypeptide component(s) (iii) and
- 15 d) optionally the secretase activity is determined in the presence of an added test substance in order to identify modulators that stimulate or inhibit the APP secretase activity.

Suitable promoters include all promoters known in the literature and familiar to the person skilled in the art that are suitable for the purpose in question.

There is to be understood by the polypeptide components mentioned in a) iii), for example, reporter domains.

In particular, a process for the quantitative and differential determination of the APP secretases involved in amyloid  $\beta$ A4 release and for the direct isolation of corresponding modulators is described which is characterised in that

- 25 a) first of all a suitable expression vector is prepared by
  - i) recombinant fusion of the secretory form of a protein, which secretory form is fused to the recognition sites for APP  $\alpha$ - or  $\beta$ -secretase, with
  - 30 ii) a suitable transmembrane anchor sequence and
  - iii) expression under the control of a suitable promoter,
- b) eukaryotic cells are stably transfected with the expression vector so produced,
- c) the transfected cells are selected with a suitable marker,
- d) the selected stable cells are analysed immunologically or enzymatically by means of the secreted reporter domain using current standard methods and finally
- 35 e) with the use of suitable vectors as negative and positive controls, the modulators that stimulate or inhibit the  $\alpha$ - or  $\beta$ -secretase activity are determined.

The expression vectors that may be used in process step a) are prepared by

- i) recombinant fusion of the secretory form of a protein (reporter), which secretory form is fused to the recognition sites for APP  $\alpha$ - or  $\beta$ -secretase, with
- ii) a suitable transmembrane anchor sequence and
- iii) expression of the protein under the control of a suitable promoter,

The expression vectors that may be used in process step a) may be, preferably, the vectors pCEP/SEAP $\alpha$ secTM1, pCEP/SEAP $\alpha$ secTM2, pCEP/SEAP $\beta$ secTM1, pCEP/SEAP $\beta$ secTM2, pCEP/SEAP $\beta$ secswTM1 and pCEP/SEAP $\beta$ secswTM2. They may also be functionally equivalent vectors.

The invention relates also to the expression vectors.

The secretory protein that may be used in process step a) may be urokinase (Langer G., Toschi L., Dieckmann J., Schleuning W.-D. (1995) Gene 161, 287-292) or preferably the secretory form of alkaline phosphatase.

The membrane or transmembrane anchor sequence that may be used in process step a) may be the transmembrane domain of any protein or, preferably, the sequences of human APLP2.

The promoter that may be used in process step a) ii) may be any eukaryotic or viral promoter, preferably the Cytomegalovirus promoter.

The cells used in process step b) are eukaryotic cells, preferably human neuroblastoma cells, especially Sy5y cells.

The present invention relates also to cells transfected with the expression vectors, such as eukaryotic cells, preferably human neuroblastoma cells, especially Sy5y cells.

The present invention relates also to the use of the transfected cells for the identification of APP secretase modulators.

The markers used in process step c) may in principle be any customary eukaryotic selection marker known to the person skilled in the art.

The selection marker preferably used in process step c) is hygromycin.

Current standard methods according to process step d) are, for example, Western blots, immunoprecipitation, enzymatic detection reactions etc..

- 5 The vectors suitable for use in process step e) are preferably, for the negative control, the vector pCEP/SEAP<sup>TM</sup> and, for the positive control, the vector pCEP/SEAP<sup>sec</sup>, or functionally equivalent vectors.

10 The invention relates also to the modulators obtainable and obtained by the process according to the invention. The modulators stimulate or inhibit the  $\alpha$ - and  $\beta$ -secretase activity.

Such modulators are, for example, compounds such as 1,1,2,2-cyclopropane tetracarbonitrile and 9,10-dihydro-12-methylene-ethane anthracen-11-one, which may be used as pharmaceutical compounds in the treatment of Alzheimer's disease.

15 The invention relates also to pharmaceutical agents or compositions that comprise at least one modulator, optionally together with formulation substances and additives customary in pharmacy.

20 The present invention relates also to pharmaceutical agents or compositions in the form of tablets, tablets with controlled release of the active ingredient, dragées, pills, capsules, film-coated tablets and film-coated tablets with controlled release of the active ingredient.

25 The pharmaceutical agents or compositions of the invention are prepared in a manner known *per se*, in a suitable dose, with the customary solid or liquid carriers or diluents and the customary pharmaceutical and commercial excipients according to the desired mode of administration. The preferred preparations are in a form suitable for oral, enteral or parenteral administration. Such forms of administration are, for  
30 example, tablets, film-coated tablets, dragées, capsules, pills, powders or depot forms and also suppositories.

Suitable tablets can be obtained, for example, by mixing the active ingredient with known excipients, for example inert diluents such as dextrose, sugars, sorbitol, mannitol, polyvinylpyrrolidone, disintegrators, such as maize starch or alginic acid,  
35 binders, such as starch or gelatin, glidants, such as magnesium stearate or talc, and/or agents for obtaining a depot effect, such as carboxypolymethylene, carboxymethyl cellulose, cellulose acetate phthalate or polyvinyl acetate. The tablets may also consist of several layers.

Correspondingly, dragées can be produced by coating cores, prepared analogously to tablets, with agents conventionally used in dragée coatings, for example polyvinylpyrrolidone or shellac, gum arabic, talc, titanium dioxide or sugars. Dragée casings may also consist of several layers, in which the excipients mentioned above for  
5 tablets may be used.

Active ingredient-containing capsules may be produced, for example, by mixing the active ingredient with an inert carrier, such as lactose or sorbitol, and encapsulating the mixture in gelatin capsules.

The modulators according to the invention may also be used, in suitable solutions,  
10 such as, for example, physiological saline, as infusion or injection solutions.

There are suitable for parenteral administration especially oily solutions, such as, for example, solutions in sesame oil, castor oil and cottonseed oil. Solubilisers, such as, for example, benzyl benzoate or benzyl alcohol, may be added to increase solubility.

15 It is also possible to incorporate the modulators obtainable and obtained by the process according to the invention into a transdermal system and thus administer them transdermally.

The modulators obtainable and obtained by the process according to the invention may be used in the treatment of Alzheimer's disease.

20 The present invention relates also to the use of the modulators obtainable by the process in the manufacture of an agent for the treatment of Alzheimer's disease and to the use of the modulators obtained by the process in the manufacture of an agent for the treatment of Alzheimer's disease.

25 The present invention relates also to a kit for the determination of the activity of APP secretase in intact cells and for the identification of modulators of APP secretase activity, which is characterised in that

- 30 a) an expression vector is prepared that comprises a DNA sequence under the control of a promoter, the DNA sequence coding for a fusion polypeptide comprising
  - i) one or more membrane anchor domains,
  - ii) one or more recognition sites for an APP secretase and
  - 35 iii) one or more polypeptide components releasable by cleavage at the recognition site,
- b) the expression vector is introduced into a cell that is capable of expressing one or more APP secretases,
- c) the APP secretase activity in the cells obtained according to step (b) is analysed based on the release of the polypeptide component(s) (iii) and



- d) optionally the secretase activity is determined in the presence of an added test substance in order to identify modulators that stimulate or inhibit the APP secretase activity.
- 5 The present invention relates especially to a kit for the quantitative and differential determination of the APP secretases involved in amyloid  $\beta$ A4 release and for the direct isolation of corresponding modulators, which is characterised in that
- a) first of all a suitable expression vector is prepared by
- 10 i) recombinant fusion of the secretory form of a protein, which secretory form is fused to the recognition sites for APP  $\alpha$ - or  $\beta$ -secretase, with
- ii) a suitable transmembrane anchor sequence and
- iii) expression under the control of a suitable promoter,
- b) eukaryotic cells are stably transfected with the expression vector so produced,
- c) the transfected cells are selected with a suitable marker,
- 15 d) the selected stable cells are analysed immunologically or enzymatically by means of the secreted reporter domain using current standard methods and finally
- e) with the use of suitable vectors as negative and positive controls, the modulators that stimulate or inhibit the  $\alpha$ - or  $\beta$ -secretase activity are
- 20 determined.

The eukaryotic cells that may be used in b) are preferably human neuroblastoma cells, especially Sy5y cells.

### Description of the drawings

- 5      **Fig. 1** shows the analysis of the C-terminal fragments after secretase activity. The cells were lysed as described below. The cell extracts were concentrated by precipitation with acetone and separated by SDS-PAGE. The proteins were transferred onto nitrocellulose. Detection was carried out with the antibody APP-CT, which is directed against the C-terminal 20 residues of APP. CT = the C-terminal APP fragment after  $\alpha$ -secretase activity.
- 10     **Fig. 2** shows the analysis of the secreted reporter fragments after secretase activity. The stably transfected cells were labelled for 2 hours with  $^{35}\text{S}$ -methionine. The conditioned medium was analysed by means of immunoprecipitation with anti-SEAP (SEAP track) or R1736 ( $\alpha$  track) and subsequent SDS-PAGE.
- 15     **Fig. 3** shows the analysis of the secreted reporter fragments after secretase activity in the presence of ammonium chloride. The stably transfected cells were pre-incubated for 40 minutes, with or without ammonium chloride, in methionine-free medium and then metabolically labelled for 2 hours, with or without ammonium chloride, with  $^{35}\text{S}$ -methionine. The conditioned medium was
- 20     analysed by means of immunoprecipitation with anti-SEAP (SEAP track) and subsequent SDS-PAGE.
- 25     **Fig. 4** shows stably transfected cells that have been sown in microtitre plates (75 000 per well) and the next day incubated for 90 minutes, with or without ammonium chloride, in cell culture medium. 30  $\mu\text{l}$  of the conditioned medium were used for quantitative analysis with SEAP measurement by chemiluminescence Phospha-Light<sup>TM</sup>, Serva) (A) or SEAP measurement by absorption (B).

To provide a better understanding of the embodiment examples forming the basis of this invention, a list has first of all been drawn up of all the procedures and methods known *per se* necessary for these experiments.

5 1. **Plasmids and vectors used**

pCEP (*in vitro* gen), APP cDNA (Kang *et al.*, (1987), Nature 325, 733-736),  
pCMV/SEAP (Berger *et al.*, (1988), Gene, 66, 1-10), pSP65-PreA4 (Dyrks *et al.*,  
(1988), EMBO Journal 7, 949-957)

10

2. **Oligonucleotide primers used**

The sequences were derived from SEAP (Berger *et al.* (1988), Gene, 66, 1-10), APP  
(Kang *et al.* (1987), Nature, 325, 733-736) and APLP2 (Wasco *et al.* (1993), Nature  
15 Genetics, 5, 95-99).

**AP5/868**

CGACTCACTA TAGGGAGACC

(Seq. ID No. 1)

20 **AP3C1a**

CCATCGATCC CCGGGTGCGC GGCCTCGG

(Seq. ID No. 2)

**bAAP/LP-2**

TTCCGACATA GTAGCAGTGC TCTCATTGGC

(Seq. ID No. 3)

25

**bALP-2/AP**

ACTGCTACTA TGTCGGAATT CTGCATCCAT

(Seq. ID No. 4)

**bCAP/LP-2**

30 AAATTGGTGC CACTGCGGGA GGA CTTCAGT

(Seq. ID No. 5)

**bCLP-2/AP**

CCGCACTGGC ACCAATTTT GATGATGAAC

(Seq. ID No. 6)

35 **APPC1a162**

CTCCTTATCG ATAATGGAGA GTTC

(Seq. ID No. 7)

**KALPC1a1**

CTGAGTATCG ATGCTCTCAT TGGCCTG

(Seq. ID No. 8)

**FAPLP2XhoI**

CCGCTCGAGC TAAATCTGCA TCTGCTCCAG (Seq. ID No. 9)

**APPClaI**

5 CGAATCGATT CAGGATATGA AGTTCAT (Seq. ID No. 10)

**aAAP/LP-2**

GTGGGTTCAA GCAGTGCTCT CATTGGCCTG (Seq. ID No. 11)

10 **aALP-2/AP**

AGCACTGCTT GAACCCACAT CTTCTGAAAA (Seq. ID No. 12)

**AB LP-2/AP**

CTCCCGCAGG AACACCAATT TTTGATGATG (Seq. ID No. 13)

15

**AB AP/LP-2**

TTGGTGTTCC TGCGGGAGGA CTTCACTCTG (Seq. ID No. 14)

**TM5**

20 GGACTAGTGG CCCACTGCGG GAGGACTTC (Seq. ID No. 15)

**TM3**

CCGCTCGAGC CTAAATCTGC ATCTGCTCCA GG (Seq. ID No. 16)

25

### 3. Cloning process

Preparation of the plasmid DNA, restriction enzyme digestion, DNA electrophoresis, DNA ligation and bacterial transformation were carried out according to methods generally known to the person skilled in the art (Sambrook *et al.*, (1989) Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor Laboratory Press, N.Y.).

30

### 4. RNA preparation

35

The cells (c.  $1 \times 10^6$ ) are washed once with PBS buffer and lysed directly in the cell culture dish by the addition of 2 ml of lysis buffer (4M guanidine thiocyanate, 25 mM sodium citrate pH 7; 100 mM  $\beta$ -mercaptoethanol, 0.5% lauroylsarcosine (v/v); 0.1% antifoam A (v/v)). After the lysed cells have been transferred into a 15 ml Sarstedt

tube, the cells are mixed for 10 seconds and 0.2 ml of sodium acetate (2M, pH 4), 2 ml of phenol (pH 4) and 0.4 ml of chloroform are added. The whole is then mixed for a further 10 seconds and centrifuged for 20 minutes (4°C, 10000 g), and the supernatant is transferred into a new Sarstedt tube. The RNA is then precipitated by adding 2 ml of isopropanol and incubating for at least one hour at -20°C. The RNA is subsequently precipitated (20 minutes, 4°C, 10000 g), and the RNA precipitate is dried, dissolved in 0.5 ml of homo-buffer and transferred into a 1.5 ml Eppendorf vessel. After repeated precipitation with isopropanol (0.5 ml isopropanol), the dried RNA is dissolved in 50-100 µl of DEPC/water.

10

## 5. RT-PCR

18 µl of commercially available Rtas mix are added to 2 µl of RNA (1 µg). Reverse transcription is then carried out: 10 min. 21°C, then 15 min. 42°C, then 5 min. 99°C and cooling to 4°C. For amplification of the cDNA, 80 µl of commercial PCR mix are added per reaction and the appropriate PCR programme is started: 5 min. 95°C; addition of 0.5 µl of Ampli-Taq-polymerase per reaction after 3.5 min. = "hot start"; followed by 30 cycles with: 1 min. 20 sec. 94°C; 1 min. 20 sec. 55°C; 1 min. 20 sec. 72°C; and a cycle for 10 min. at 72°C, after which the samples are cooled to 4°C.

20

### 5.1 PCR

25 The PCR reactions were carried out as follows:

	recommended conc.	µl
per		100 µl
DEPC/water		75
10 times buffer Taq or Pfu		10
dNTP 2.5 mM	200 µM	8
µl primer 1	50 pmol 0.5 µM	2.5
µl primer 2	50 pmol 0.5 µM	2.5
µl template	(0.1-250 ng) 40 ng	1
Taq /Pfu 2.5 U/µl	2.5 U/100 µl	1

Cycles: 25

denaturation	1 min. 95°C
annealing	1 min. 55°C
extension	2 min. 72°C
final extension	5 min. 72°C

## 5 6. Cell culture and transfection:

The sub-clone of the neuroblastoma cell line SH-Sy5y was cultured in equal amounts of minimal essential medium (MEM, with Earle's salts and L-glutamine) and Ham's F-12, supplemented with non-essential amino acids (Eagle's formulation), penicillin  
10 (50 U/ml), streptomycin (40 µg/ml) and 10 % (v/v) foetal calf serum (FCS).

For stable transfection, 5 times 10<sup>5</sup> cells were sown on 60 mm dishes and incubated overnight at 37°C. Once the cells had achieved approximately 80 % confluence, they were transfected by means of lipofectin. For that purpose the cells were washed three times with Opti-MEM I before the DNA/lipofectin solution was added. The  
15 DNA/lipofectin solution was prepared beforehand by mixing diluted DNA (10-20 µg of DNA in 1.5 ml of Opti-MEM) and diluted lipofectin (30-50 µg of lipofectin in 1.5 ml of Opti-MEM) and incubated for 30 minutes at room temperature. After an incubation of 8 hours at 37°C, the cells were cultured in culture medium for a further 24-48 hours and stable lines were selected by the addition of hygromycin B (400 µg/ml the first  
20 week, then 300 µg/ml).

## 7. Metabolic labelling of cell cultures and preparation of cell lysates

25 After removal of the culture medium, the cells were preincubated for 40 minutes with 2 ml of MEM (6 cm dish) without methionine. The labelling of the cells was carried out with 300 µCi of [<sup>35</sup>S] methionine in 1.5 ml of MEM without methionine for 2-3 hours. The medium (conditioned medium) was then collected, and the cells were washed with PBS at 4°C and scraped off the dish. For lysis, the centrifuged-off cells were  
30 resuspended in 600 µl of sol-buffer (50 mM tris-HCl [pH7.5], 150 mM NaCl, 2 mM EDTA, 1% Triton X-100 and commercial protease-inhibitor cocktail ) and incubated for 30 minutes on ice. The cell nuclei were centrifuged off at 10000 x g for 5 minutes. The supernatant (cell lysate) was stored at -20°C for further analysis.

## 8. Immunoprecipitation

The immunoprecipitation was carried out according to the method of Anderson *et al.* (Methods Enzymol. 96, 110-120).

- 5 For the immunoprecipitation, the conditioned medium was standardised on 50 mM tris-HCl [pH 7.5], 150 mM NaCl, 2 mM EDTA, 1% Triton X-100 and commercial protease-inhibitor cocktail. For the preincubation, the conditioned medium and the cell lysate were incubated for 30 minutes with 5  $\mu$ l of pre-immunoserum and 50  $\mu$ l (5 mg) of protein A/Sepharose. The samples were briefly centrifuged and the supernatants
- 10 incubated overnight at 4°C with antibody (10  $\mu$ l of SEAP, 5  $\mu$ l of A4CT) and 50  $\mu$ l (5mg) of protein A/Sepharose. The antibody-protein A complexes were washed three times with washing buffer A (10 mM tris-HCl [pH 7.5], 150 mM NaCl, 0.2 % Triton X-100, 2 mM EDTA), twice with washing buffer B (10 mM tris-HCl [pH 7.5], 500 mM NaCl, 0.2 % Triton X-100, 2 mM EDTA) and once with washing buffer C (10 mM tris-
- 15 HCl [pH 7.5]) and then incubated twice in Laemmli test buffer for 5 minutes at 100°C. The analysis of the labelled proteins was carried out by means of tris-tricine SDS-PAGE and phosphoimaging.

## 20 9. Tris-tricine-SDS-polyacrylamide gel electrophoresis

The gel electrophoresis was carried out according to Schägger and Jagow ((1987) Analytical Biochemistry 166, 368-379).

25

## 10. Precipitation with acetone

- 200  $\mu$ l of the cell lysate are incubated with 1 ml of acetone for 30 minutes at -40°C and then centrifuged off for 10 minutes at 13000 rpm; the supernatant is discarded
- 30 and the pellet is dried at 37°C. The precipitated protein is dissolved in 40  $\mu$ l of 8M urea for 15 minutes at 56°C, 40  $\mu$ l of Laemmli test buffer are added twice and the whole is incubated for a further 15 minutes at 56°C for the purpose of denaturation.

## 35 11. Western Blot Analysis

When the gel electrophoresis is complete, the gel is washed for 30 minutes in transfer buffer (25 mM tris, 192 mM glycine, 0.05 % SDS, 20% methanol). The proteins are for 2.5 hours electrophoretically transferred (60 V, 280 mA, 4°C) in transfer buffer onto

0.45  $\mu$ m of nitrocellulose. After saturation of the nitrocellulose filter in TBST/powdered milk (20 mM tris/pH 7.6, 127 mM NaCl, 0.5% Tween 20, 1% powdered milk) for at least 1 hour at room temperature (RT), the filter is washed twice with TBST (20 mM tris/pH 7.6, 127 mM NaCl, 0.5% Tween 20®) and incubated for a further hour (1-16  
5 hours depending on antibody) at RT with the primary antibody in TBST/powdered milk. After washing three times with TBST, incubation is carried out for at least 30 minutes at RT with secondary antibody (1:7500), coupled to peroxidase, in TBST/powdered milk, followed by washing a further three times with TBST and development with a commercial ECL kit.

10

## 12. SEAP Assay: SEAP measurement by chemiluminescence

All steps are carried out in 96-well microtitre plates. One day before the analysis, 75 000 cells are sown per 96 wells. The analysis is carried out in 200  $\mu$ l of culture  
15 medium plus/minus test substance for from 1 to 20 hours at 37°C. Subsequently, 90  $\mu$ l of dilution buffer (0.05M tris-HCl, pH 7.4; 0.15M NaCl) are added to 30  $\mu$ l of the medium and the whole is incubated for 60 minutes at 65°C. After 2 minutes on ice, 100  $\mu$ l of the heat-treated medium have 100  $\mu$ l of assay buffer (2M diethanolamine, pH 7.8, 1 mM MgCl<sub>2</sub>, 20 mM L-homoarginine) added, and the whole is incubated at  
20 room temperature for 5 minutes. 100  $\mu$ l of reaction buffer (0.1M diethanolamine, CSPD) are added to the incubate and, after 20 minutes, the chemiluminescence is measured for 5 seconds in a luminometer.

## 25 13. SEAP Assay: SEAP measurement by absorption

All steps are carried out in 96-well microtitre plates. One day before the analysis, 75 000 cells are sown per 96 wells. The analysis is carried out in 200  $\mu$ l of culture medium with and without test substance for from 1 to 20 hours at 37°C.  
30 Subsequently, 100  $\mu$ l of the medium are incubated at 65°C for 60 minutes. After 2 minutes on ice, 100  $\mu$ l of the heat-treated medium have 100  $\mu$ l of assay buffer (2M diethanolamine, pH 7.8, 1 mM MgCl<sub>2</sub>, 20 mM L-homoarginine) and 20  $\mu$ l of p-nitrophenol phosphate (120 mM in assay buffer) added. The evaluation is carried out in an ELISA reader at OD 405 as terminal point determination or as kinetics, the  
35 amount of enzyme being calculated as follows: 1 mU SEAP = 0.04 A405 increase/min.



The following embodiment Examples illustrate the invention without the invention being limited thereto :

5     **Example 1**

**Preparation of the cloning and expression vectors**

**1.1    Vector pBC/SEAP**

10

The N-terminal 511 amino acids of the secretory form of human placental alkaline phosphatase (SEAP; human from the placenta, Berger *et al.* (1988), Gene, 66, 1-10) were amplified by means of PCR from the pCMV/SEAP expression vector (Tropix, Serva, Cat.No. AV10C) as template and the oligonucleotide primers AP5/868 and AP3Cla, and cloned by way of Hind 3 / Cla I into pBluescript SK. The vector  
15    pBC/SEAP is obtained.

**1.2    Vector SP65/APLP2-CT**

20

The C-terminal 82 amino acids of human APLP2 (Wasco *et al.*, (1993), Nature genetics 5, 95-99) were amplified by means of the above-described RT-PCR and subsequent PCR with the specific oligonucleotide primers TM5 and TM3 and cloned by way of SpeI/XhoI into Sp65/preA4, the vector SP65/APLP2-CT being obtained.

25

**1.3    Vector pCEP/SEAP $\alpha$ secTM1**

The APP fragment , amino acids 604 to 622, referred to here as  $\alpha$ sec (numbering  
30    according to APP695), was amplified by means of PCR from APP cDNA (Kang *et al.*, (1987), Nature 325, 733-736) as template and the oligonucleotide primers APPClaI and aALP-2/AP. Then, the C-terminal 72 amino acids of APLP2 (Wasco *et al.*, (1993), Nature genetics 5, 95-99), referred to here as TM1, were amplified by means of PCR from vector SP65/APLP2-CT as template and the oligonucleotide primers aAAP/LP-2  
35    and FAPLP2XhoI. The APP fragment and the APLP2 fragment were then fused by means of PCR with the oligonucleotide primers APPClaI and FAPLP2XhoI. The resulting APP/APLP2 hybrid molecule was cloned by way of ClaI / Xho I into pBC/SEAP, vector pBCSEAP $\alpha$ secTM being obtained. For cellular expression, the

resulting fusion fragment SEAP $\alpha$ secTM was cloned by way of Hind3/XhoI into the expression vector pCEP4.

#### 5 1.4 Vector pCEP/SEAP $\alpha$ secTM2

The APP fragment, amino acids 604 to 615, referred to here as  $\alpha$ sec (numbering according to APP695) was amplified by means of PCR from APP cDNA (Kang *et al.*, (1987), Nature, 325, 733-736) as template and the oligonucleotide primers APPClal and aBLP-2/AP.

10 Subsequently, the C-terminal 80 amino acids of APLP2 (Wasco *et al.*, (1993), Nature genetics 5, 95-99), referred to here as TM2, were amplified by means of PCR from the vector SP65/APLP2-CT as template and the oligonucleotide primers aBAP/LP-2 and FAPLP2XhoI.

15 The APP fragment and the APLP2 fragment were then fused with the oligonucleotide primers APPClal and FAPLP2XhoI by means of PCR. The resulting APP/APLP2 hybrid molecule was cloned by way of Clal / Xho I into the vector pBC/SEAP resulting in the vector pBCSEAP $\alpha$ secTM2.

For cellular expression, the resulting fusion fragment SEAP $\alpha$ secTM was cloned by  
20 way of Hind3/XhoI into the expression vector pCEP4.

#### 1.5 Vector pCEP/SEAP $\beta$ secTM1

25 The APP fragment with the amino acids 535 to 604, referred to here as  $\beta$ sec, (numbering according to APP695), was amplified by means of PCR from APP cDNA (Kang *et al.*, (1987), Nature, 325, 733-736) as template and the oligonucleotide primers APPClal62 and bALP-2/AP. Then, the C-terminal 72 amino acids of APLP2 (Wasco *et al.*, (1993), Nature genetics 5, 95-99), referred to here as TM2, were  
30 amplified by means of PCR from the vector SP65/APLP2-CT as template and the oligonucleotide primers bAAP/LP-2 and FAPLP2XhoI. The APP fragment and the APLP2 fragment were then fused with the oligonucleotide primers APPClal62 and FAPLP2XhoI by means of PCR. The resulting APP/APLP2 hybrid molecule was  
cloned by way of Clal / Xho I into pBC/SEAP, resulting in the vector  
35 pBCSEAP $\beta$ secTM1. For cellular expression, the resulting fusion fragment SEAP $\beta$ secTM1 was cloned by way of Hind3/XhoI into the expression vector pCEP4.

### 1.5a Vector pCEP/SEAP $\beta$ secswTM1

Vector pCEP/SEAP $\beta$ secswTM1 was generated analogously to pCEP/SEAP $\beta$ secTM1 using APP751sw (Urmoneit *et al.* 1995, Journal of Molecular Neuroscience, Vol. 6, 23-32) instead of APP cDNA as template.

### 1.6 Vector pCEP/SEAP $\beta$ secTM2

The APP fragment, amino acids 535 to 614, referred to here as  $\beta$ sec, (numbering according to APP695), was amplified by means of PCR from APP cDNA (Kang *et al.*, (1987), Nature, 325, 733-736) as template and the oligonucleotide primers APPClal62 and bCLP-2/AP. Then, the C-terminal 81 amino acids of APLP2 (Wasco *et al.*, (1993), Nature genetics 5, 95-99), referred to here as TM2, were amplified by means of PCR from the fragment SP65/APLP2-CT as template and the oligonucleotide primers bCAP/LP-2 and FAPLP2XhoI. The APP fragment and the APLP2 fragment were then fused with the oligonucleotide primers APPClal62 and FAPLP2XhoI by means of PCR and the resulting APP/APLP2 hybrid molecule was cloned by way of Clal / Xho I into pBC/SEAP. The vector pBCSEAP $\beta$ secTM2 was obtained. For cellular expression, the resulting fusion fragment SEAP $\beta$ secTM2 was cloned by way of Hind3/XhoI into the expression vector pCEP4.

### 1.6a Vector pCEP/SEAP $\beta$ secswTM2

Vector pCEP/SEAP $\beta$ secswTM2 was generated analogously to pCEP/SEAP $\beta$ secTM2 using APP751sw (Urmoneit *et al.* 1995, Journal of Molecular Neuroscience, Vol. 6, 23-32) instead of APP cDNA as template.

### 1.7 Vector pCEP/SEAPTM

The C-terminal 70 amino acids of APLP2 (Wasco *et al.*, (1993), Nature genetics 5, 95-99), referred to here as TM, were amplified by means of PCR from SP65/APLP2-CT as template and the oligonucleotide primers KALPClal and FAPLP2XhoI and cloned by way of Clal / Xho I into pBC/SEAP, resulting in the vector pBCSEAPTM. For cellular expression, the resulting fusion fragment SEAPTM was cloned by way of Hind3/XhoI into the expression vector pCEP4.

### 1.8 Vector pCEP/SEAPsec

The Hind III / Xba I fragment from the pCMV/SEAP expression vector (Tropix, Serva, Cat. No. AV10C), coding for the secretory form of human placental alkaline phosphatase (SEAP; human from the placenta, Berger *et al.* (1988), Gene, 66, 1-10) was intermediately cloned into pBluescript SK and then cloned by way of Hind3/NotI into the expression vector pCEP4.

### 10 Example 2

#### Transfection of human neuroblastoma cells Sy5y

Sy5y cells are transfected with the above-described expression vectors. On account of the episomal character of the expression vectors, a stable expression is achieved not by dilution and cloning but simply by selection with hygromycin. Analysis of the stable cells is effected both immunologically (immunoprecipitation with SEAP and APP antibodies) and by means of enzymatic detection of the secreted reporter (SEAP assay).

The stably transfected cells release the reporter (SEAP) into the medium only after  $\alpha$  or  $\beta$ -secretase activity. The amount of secreted reporter reflects the level of the respective proteolytic activity. The amount of released reporter can be measured by current standard methods, such as, for example, chemiluminescence, down to sub-nanomolar concentrations. The sensitivity achieved thereby allows a quantitative determination of the  $\alpha$  or  $\beta$ -secretase activity in the "high capacity screen"-compatible 96-well format. Published  $\alpha$  and  $\beta$ -secretase modulators, such as, for example, phorbol ester and  $\text{NH}_4\text{Cl}$ , exhibit the expected effects in the system described herein. The above-mentioned positive control (pCEP/SEAPsec) and negative control (pCEP/SEAPTM) confer on the system an additional specificity since, as a result, in the course of an HCS falsely positive compounds can easily be identified by secondary screening (inhibition of the secretion caused by a generally toxic influence and inhibition of the alkaline phosphatase is identified by cells transfected with pCEP/SEAPsec; stimulation of the secretion caused by membrane instability is identified by cells transfected with pCEP/SEAPTM).

**Example 3****Verification of the processing of the reporter fusion constructs by the corresponding secretase activities**

5 The secretase activities generate, starting from physiological membrane-bound APP, various extracellularly secreted N-terminal fragments (APPsec $\alpha$ , APPsec $\beta$  and APPsec $\gamma$ ) and the corresponding intracellular membrane-bound C-terminal fragments (APPsec $\alpha$   $\Rightarrow$  CT; APPsec $\beta$   $\Rightarrow$  A4CT; APPsec $\gamma$   $\Rightarrow$  CT-A4). Provided processing is

10 correct, the expression of the reporter fusion constructs should, after the respective secretase activity, result in a secreted N-terminal fragment (SEAP) and the corresponding intracellular, membrane-bound C-terminal fragment.

Fig. 1 shows a Western blot analysis, developed with an antibody to the C-terminus of APP/APLP2 (anti-APP-CT (Dr. Mönning Schering AG)). Compared with the control

15 CEP (pCEP transfected cells) both the SEAPsec $\alpha$ TM2 and the SEAPsec $\beta$ TM1 cells exhibit an additionally generated C-terminal fragment which, on account of its size, runs just below the CT fragment of the endogenous APP (CT in the CEP tracks). The corresponding secreted N-terminal fragment can be seen in Fig. 2 after immuno-

precipitation with an antibody to SEAP. In addition to the identification of the secreted

20 reporter, Fig. 2 also exhibits proof for the sequence-specific processing of the SEAPsec $\alpha$ TM constructs. The antibody R1736 (Dr. Selkoe/Dr. Haass, Brigham and Woman's Hospital, 221 Long Wood Ave, Boston, MA 02119) recognises the C-

terminal amino acid of APP, which is released after  $\alpha$ -secretase activity. Immuno-

reactivity with R1736 thus indicates sequence-specific  $\alpha$ -secretase activity. As can be

25 seen in Fig. 2, track  $\alpha$ , only the SEAPsec $\alpha$ TM1 and SEAPsec $\alpha$ TM2 cells secrete significant amounts of SEAP with the R1736 epitope. The small secretion of SEAP with the R1736 epitope in the case of the SEAPsec $\beta$ TM2 cells results in a residual activity of  $\alpha$ -secretase compared with the mutagenised recognition sequence (for details see above under expression vectors). The reporter fusion construct without

30 secretase recognition site (SEAPTM= negative control) shows no reporter activity in the medium.

#### Example 4

##### Verification of the regulation of the secretase activities with the fusion constructs as substrate

5 It is known that  $\beta$ -secretase activity can be inhibited by compounds that render alkaline endosomal/lysosomal compartments ( $\text{NH}_4\text{Cl}$ , chloroquine, methylamine etc.), whilst the  $\alpha$ -secretase activity is not affected by those conditions. Fig. 3 shows an immunoprecipitation of the medium with SEAP-antibody after metabolic labelling in  
10 the presence or absence of 20 mM  $\text{NH}_4\text{Cl}$ . It can be seen clearly that the processing of SEAPsec $\beta$ TM2 but not of SEAPsec $\alpha$ TM1 is inhibited under those conditions. In addition to the immunological analysis of the specific regulation of the reporter fusion constructs, the modulation of the reporter secretion was determined quantitatively by means of the SEAP assay.  
15 In contrast to  $\text{NH}_4\text{Cl}$ , phorbol ester (PMA) stimulates  $\alpha$ -secretase activity without having an effect on  $\beta$ -secretase activity. It was also possible for that secretase-specific regulation to be reproduced with the reporter fusion constructs. Fig. 4 shows an SEAP assay in which the secreted SEAP was measured as a function of phorbol ester (Fig. 4A) and  $\text{NH}_4\text{Cl}$  (Fig. 4B). The secretion of SEAP in the case of the  
20 SEAP $\alpha$ TM cells can be stimulated by PMA by approximately 400%, which agrees very well with the hitherto published data. Under those conditions no, or only a slight stimulation, is observed in the case of the secretion control (SEAPsec cells) and the SEAPsec $\beta$ TM cells. Also, the specific inhibition of  $\beta$ -secretase activity in the presence of  $\text{NH}_4\text{Cl}$  is reproduced as shown by the SEAP assay in Fig. 4.

25

#### Example 5

##### Overview of the substances tested in the SEAP assay

30

Using the cellular test system, various compounds were examined for their activity during the processing of the reporter fusion constructs. The substances tested in the SEAP assay were divided into different classes as shown in the following Table.

Substance	Incubation	Effect on the processing of sec-fusion proteins
<b>Acetylcholinesterase inhibitors</b>	2 h, 5 h, 16 h	
Tacrin	10-30 $\mu$ M	at 30 $\mu$ M 20-30 % inhibition of the SEAP secretion in all constructs
Gаланthamin	10-30 $\mu$ M	no effect
Physostigmin	10-30 $\mu$ M	no effect
<b>Growth factors</b>	1-22 h	
PDGF	50 ng/ml	no effect, no action on starved cells
NGF	50 ng/ml	no effect
bFGF	5-50 ng/ml, 4 h	no effect
IGF-1	100 ng/ml, 2 h	no effect
EGF	100 ng/ml, 2 h	no effect
<b>Protease inhibitors</b>	1-2 h	
Pefabloc	200-400 $\mu$ M	no effect
Aprotinin	0.02-2 $\mu$ g/ml	no effect
Pepstatin	15 $\mu$ M, 70* $\mu$ M	no effect
Leupeptin	10-100 $\mu$ M	no effect
Phenanthroline	5-500* $\mu$ M, 3 h	50 $\mu$ M inhibits SEAP secretion of all constructs by ~30 %
CGA	0.1-10 $\mu$ M, 2 h, 5 h	no effect
Phosphoramidon	2, 20 $\mu$ M	no effect
NH <sub>4</sub> Cl	10 mM, 2.5 h	inhibits SEAP secretion of SEAP $\beta$ sec and SEAP $\beta$ secsw by ~40 %
BafilomycinA1	0.2 $\mu$ M	inhibits SEAP secretion of SEAP $\beta$ sec and SEAP $\beta$ secsw by ~35 %
Methylamine	10-30 mM	inhibits SEAP secretion of SEAP $\beta$ sec and SEAP $\beta$ secsw by ~40 %
<b>Cytokine</b>	2 h	
IL-1 $\beta$	10 ng/ml	no effect on SEAP $\beta$ sec1
IL-4	10 ng/ml	~20 % inhibition of SEAP secretion in all constructs
TNF- $\alpha$	200 ng/ml	~30 % inhibition of SEAP secretion in all constructs
Con.medium Mikrogliia	-/+ LPS stim.	no effect
arachidonic acid	0.3-3 $\mu$ M	no effect

Substance	Incubation	Effect on the processing of sec-fusion proteins
<b>Inhibitors in the signal transduction</b>	1-3 h	
D609 (PC-PLC-g) Wortmannin (PI-3-kinase) Gö6850, Gö6976 (PKC)	0.2-20* µg/ml 0.1*, 1* µM, 1 h 1 µM, 1.5 h	no effect no effect ~80 % inhibition of the TPA induced SEAP secretion in the case of SEAP $\alpha$ sec1
<b>Activators in the signal transduction</b>	1-3 h	
Carnachol (M-receptor) TPA (PKC)	1 mM 0.16, 0.2 µM	increases secretion of SEAP in the case of SEAP $\alpha$ sec approx. twofold increases secretion of SEAP in the case of SEAP $\alpha$ sec approx. two- to four-fold
BMBF305 Forskolin (AC)	0.1-3* µg/ml 0.5, 1 µM 3 h preincubation	increases secretion of SEAP in the case of SEAP $\alpha$ sec1 preincubation with Forskolin inhibits TPA-induced secretion in the case of SEAP $\alpha$ sec1 by ~50 %
<b>Oxidative Stress</b>	1-3 h	
Dithiocarbamate (SOD)	0.1-10 µM, 3 h	no effect
H <sub>2</sub> O <sub>2</sub>	10-100 µM	no effect

For each substance group, the range for the incubation time for all substances of the group is quoted, with incubation times that differ therefrom being noted after the amount. Concentrations marked with \* resulted in a visually detectable change in the morphology of the Sy5y cells.

Key :

SEAP $\alpha$ sec: corresponds to SEAP $\alpha$ secTM1 and SEAPsec $\alpha$ TM2

SEAP $\alpha$ sec1: corresponds to SEAPsec $\alpha$ TM1

SEAP $\alpha$ sec2: corresponds to SEAPsec $\alpha$ TM2

SEAP $\beta$ sec: corresponds to SEAP $\beta$ secTM1 and SEAP $\beta$ secTM2

SEAP $\beta$ sec1 : corresponds to SEAPsec $\beta$ TM1

SEAP $\beta$ sec2: corresponds to SEAPsec $\beta$ TM2

SEAP $\beta$ secsw: corresponds to SEAP $\beta$ secswTM1 and SEAP $\beta$ secswTM2

SEAP $\beta$ secsw1 : corresponds to SEAPsec $\beta$ swTM1

SEAP $\beta$ secsw2: corresponds to SEAPsec $\beta$ swTM2



**Example 6**

Detection of pharmacological modulators using the process according to the invention and the plasmids and cells according to the invention

5

The process according to the invention is used as described above for screening for pharmacological modulators of amyloid  $\beta$ A4 release.

The following compounds could be found as modulators

1,1,2,2-cyclopropane tetracarbonitrile (1) and

10 9,10-dihydro-12-methylene-ethane anthracen-11-one (2)

Compound (1) and its preparation are described by Wideqvist (Ark. Kemi, 20 B No. 4, p 6, 1945) and Hart *et al.* (J. Org. Chem. 31, 2784-2789, 1966).

Compound (2) and its preparation is described by E. Snyder (J. Org. Chem. 25, 1328-1330, 1960), Hart *et al.* (J. Amer. Chem. Soc., 95, 6294, 1973) and Varecht *et al.* (J.

15 Chem. Res. Miniprint, 1979).

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

5

## (i) APPLICANT:

- (A) NAME: Schering Aktiengesellschaft
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15

- (ii) TITLE OF INVENTION: Process for the determination of APP secretase modulators and the use thereof as agents in the treatment of Alzheimer's disease

20

## (iii) NUMBER OF SEQUENCES: 16

## (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- 25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

## (vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: DE 19641180.7
- 30 (B) FILING DATE: 24-SEP-1996

## (2) INFORMATION FOR SEQ ID NO: 1:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CGACTCACTA TAGGGAGACC

## 45 (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

CCATCGATCC CCGGGTGCGC GCGGTCGG

(2) INFORMATION FOR SEQ ID NO: 3:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TTCCGACATA GTAGCAGTGC TCTCATTGGC

20

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

30

ACTGCTACTA TGTCGGAATT CTGCATCCAT

(2) INFORMATION FOR SEQ ID NO: 5:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AAATTGGTGC CACTGCGGGA GGACTTCAGT

45 (2) INFORMATION FOR SEQ ID NO: 6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CCGCAGTGGC ACCAATTTTT GATGATGAAC

## (2) INFORMATION FOR SEQ ID NO: 7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CTCCTTATCG ATAATGGAGA GTTC

## (2) INFORMATION FOR SEQ ID NO: 8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CTGAGTATCG ATGCTCTCAT TGGCCTG

## (2) INFORMATION FOR SEQ ID NO: 9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CCGCTCGAGC TAAATCTGCA TCTGCTCCAG

## (2) INFORMATION FOR SEQ ID NO: 10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CGAATCGATT CAGGATATGA AGTTCAT

## (2) INFORMATION FOR SEQ ID NO: 11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GTGGGTTCAA GCAGTGCTCT CATTGGCCTG

## (2) INFORMATION FOR SEQ ID NO: 12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

AGCACTGCTT GAACCCACAT CTTCTGAAAA

## (2) INFORMATION FOR SEQ ID NO: 13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CTCCCGCAGG AACACCAATT TTTGATGATG

(2) INFORMATION FOR SEQ ID NO: 14:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

TTGGTGTTCC TGC GGGAGGA CTTCAGTCTG

15 (2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

25 GGACTAGTGG CCCACTGCGG GAGGACTTC

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CCGCTCGAGC CTAAATCTGC ATCTGCTCCA GG

**Patent Claims**

1. Process for the determination of the activity of APP secretase in intact cells and for the identification of modulators of APP secretase activity, characterised in that
- 5           a) an expression vector is prepared that comprises a DNA sequence under the control of a promoter, the DNA sequence coding for a fusion polypeptide comprising
- 10           i) one or more membrane anchor domains,
- ii) one or more recognition sites for an APP secretase and
- iii) one or more polypeptide components releasable by cleavage at the recognition site,
- b) the expression vector is introduced into a cell that is capable of expressing one or more APP secretases,
- 15           c) the APP secretase activity in the cells obtained according to step (b) is analysed based on the release of the polypeptide component(s) (iii) and
- d) optionally the secretase activity is determined in the presence of an added test substance in order to identify modulators that stimulate or inhibit the APP secretase activity.
- 20
2. Process for the quantitative and differential determination of the APP secretases involved in amyloid  $\beta$ A4 release and for the direct isolation of corresponding modulators, characterised in that
- a) first of all a suitable expression vector is prepared by
- 25           i) recombinant fusion of the secretory form of a protein, which secretory form is fused to the recognition sites for APP  $\alpha$ - or  $\beta$ -secretase, with
- ii) a suitable transmembrane anchor sequence and
- iii) expression under the control of a suitable promoter,
- b) eukaryotic cells are stably transfected with the expression vector so produced,
- 30           c) the transfected cells are selected with a suitable marker,
- d) the selected stable cells are analysed immunologically or enzymatically by means of the secreted reporter domain using current standard methods and finally
- e) with the use of suitable vectors as negative and positive controls, the
- 35           modulators that stimulate or inhibit the  $\alpha$ - or  $\beta$ -secretase activity are determined.

3. Process according to claim 2, characterised in that, in accordance with step b) human neuroblastoma cells are stably transfected with the expression vector so produced.
- 5 4. Process according to claim 1 or 2, characterised in that the expression vectors that may be used in process step a) are the vectors pCEP/SEAP $\alpha$ secTM1, pCEP/SEAP $\alpha$ secTM2, pCEP/SEAP $\beta$ secTM1, pCEP/SEAP $\beta$ secTM2, pCEP/SEAP $\beta$ secswTM1 and pCEP/SEAP $\beta$ secswTM2.
- 10 5. Process according to any one of claims 2 to 4, characterised in that the secretory protein that may be used in process step a) i) is the secretory form of alkaline phosphatase or urokinase.
- 15 6. Process according to any one of claims 2 to 5 characterised in that the transmembrane anchor sequences that may be used in process step a) ii) are the sequences of human APLP2.
- 20 7. Process according to any one of claims 2 to 6, characterised in that the promoter that may be used in process step a) iii) renders possible expression in eukaryotic systems.
- 25 8. Process according to any one of claims 2 to 7, characterised in that the promoter that may be used in process step a) iii) is a eukaryotic or viral promoter.
9. Process according to any one of claims 2 to 8, characterised in that the promoter that may be used in process step a) iii) is the Cytomegalovirus promoter.
- 30 10. Process according to any one of claims 1 to 9, characterised in that the cells used in process step b) are Sy5y cells.
11. Process according to any one of claims 2 to 10, characterised in that the selection marker used in process step c) is hygromycin.
- 35 12. Process according to any one of claims 2 to 11, characterised in that the vectors suitable for use in process step e) are, for the negative control, the vector pCEP/SEAPTM and, for the positive control, the vector pCEP/SEAPsec.



13. Modulator, obtainable in accordance with the process according to any one of claims 1 to 12.
14. Modulator, obtained in accordance with the process according to any one of claims 1 to 12.
15. Modulator according to claim 13 or 14, characterised in that it is the compound 1,1,2,2-cyclopropane tetracarbonitrile or 9,10-dihydro-12-methylene-ethane anthracen-11-one.
16. Pharmaceutical agent, comprising at least one modulator according to any one of claims 13 to 15 with customary formulation substances and additives.
17. Pharmaceutical agent according to claim 16, for the treatment of Alzheimer's disease.
18. Use of a modulator obtainable by the process according to any one of claims 1 to 15 in the manufacture of an agent for the treatment of Alzheimer's disease.
19. Use of a modulator obtained by the process according to any one of claims 1 to 15 in the manufacture of an agent for the treatment of Alzheimer's disease.
20. Expression vector prepared by
- i) recombinant fusion of the secretory form of a protein (reporter), which secretory form is fused to the recognition sites for APP  $\alpha$ - or  $\beta$ -secretase, with
  - ii) a suitable transmembrane anchor sequence and
  - iii) expression of the protein under the control of a suitable promoter.
21. Expression vector according to claim 20, characterised in that the vector is pCEP/SEAP $\alpha$ secTM1, pCEP/SEAP $\alpha$ secTM2, pCEP/SEAP $\beta$ secTM1, pCEP/SEAP $\beta$ secTM2, pCEP/SEAP $\beta$ secswTM1 or pCEP/SEAP $\beta$ secswTM2.
22. Cell, transfected with an expression vector according to claim 20 or 21.
23. Human neuroblastoma cell, transfected with an expression vector according to claim 20 or 21.
24. Sy5y cell, transfected with an expression vector according to claim 20 or 21.

25. Use of the transfected cells according to any one of claims 22 to 24 in the identification of APP secretase modulators.
- 5 26. Kit for the determination of the activity of APP secretase in intact cells and for the identification of modulators of APP secretase activity, characterised in that
- a) an expression vector is prepared that comprises a DNA sequence under the control of a promoter, the DNA sequence coding for a fusion polypeptide comprising
- 10 i) one or more membrane anchor domains,  
ii) one or more recognition sites for an APP secretase and  
iii) one or more polypeptide components releasable by cleavage at the recognition site,
- b) the expression vector is introduced into a cell that is capable of expressing one or more APP secretases,
- 15 c) the APP secretase activity in the cells obtained according to step (b) is analysed based on the release of the polypeptide component(s) (iii) and  
d) optionally the secretase activity is determined in the presence of an added test substance in order to identify modulators that stimulate or inhibit the APP secretase activity.
- 20 27. Kit, according to claim 26, for the quantitative and differential determination of the APP secretases involved in amyloid  $\beta$ A4 release and for the direct isolation of corresponding modulators, characterised in that
- 25 a) first of all a suitable expression vector is prepared by
- i) recombinant fusion of the secretory form of a protein, which secretory form is fused to the recognition sites for APP  $\alpha$ - or  $\beta$ -secretase, with
- ii) a suitable transmembrane anchor sequence and
- iii) expression under the control of a suitable promoter,
- 30 b) eukaryotic cells are stably transfected with the expression vector so produced,  
c) the transfected cells are selected with a suitable marker,  
d) the selected stable cells are analysed immunologically or enzymatically by means of the secreted reporter domain using current standard methods and finally
- 35 e) with the use of suitable vectors as negative and positive controls, the modulators that stimulate or inhibit the  $\alpha$ - or  $\beta$ -secretase activity are determined.

28. Kit, according to claim 27, characterised in that in b) human neuroblastoma cells are stably transfected with the expression vector so produced.
29. Kit, according to claim 27, characterised in that in b) Sy5y cells are stably transfected.

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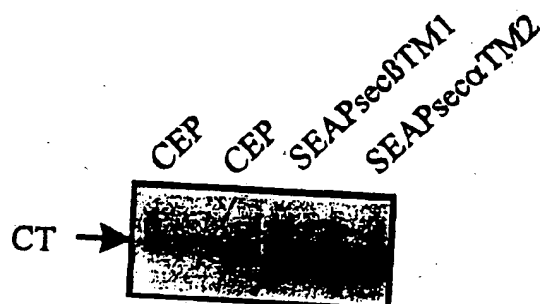


Fig. 1

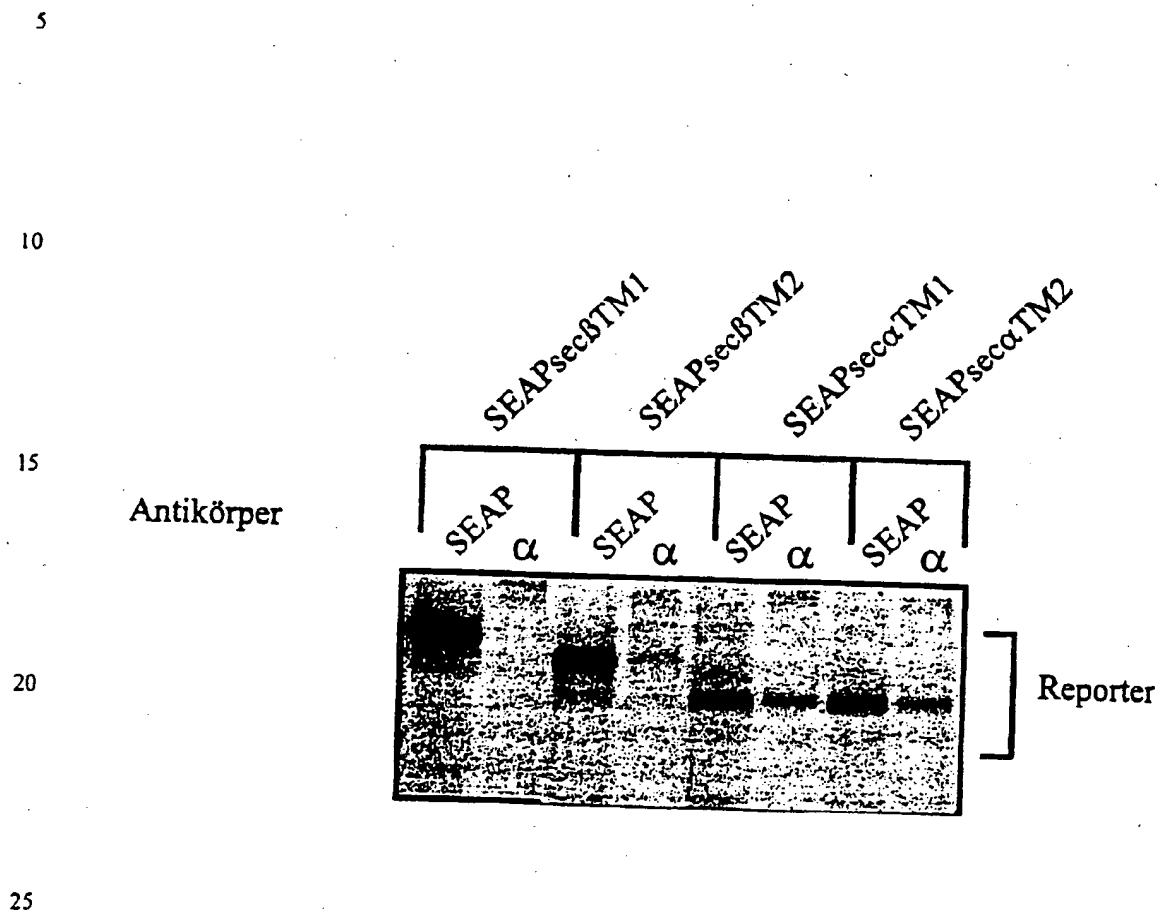


Fig. 2

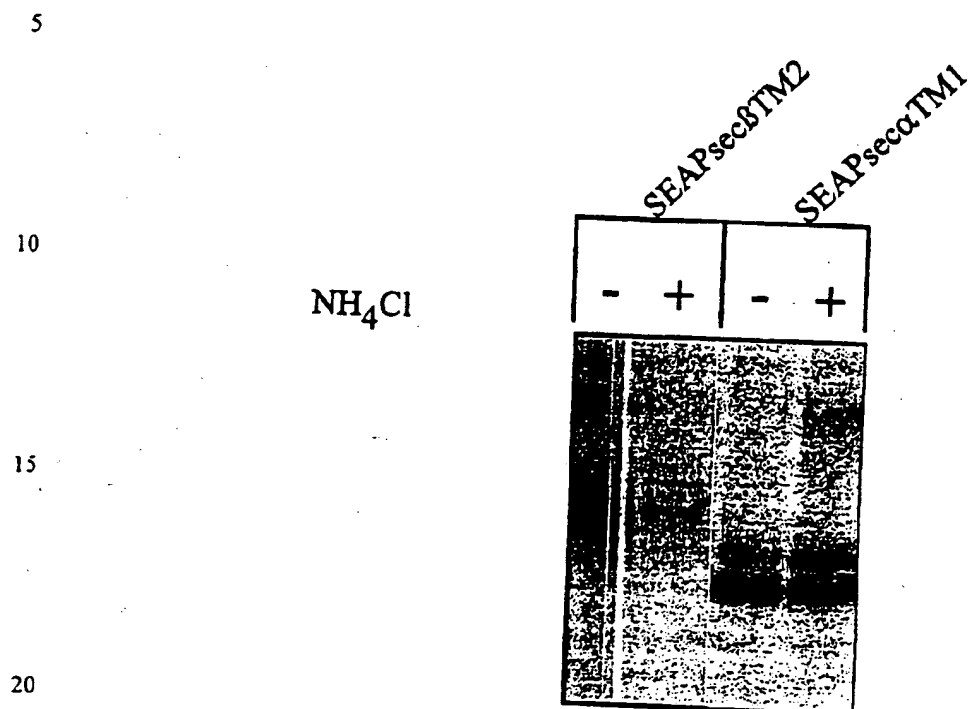
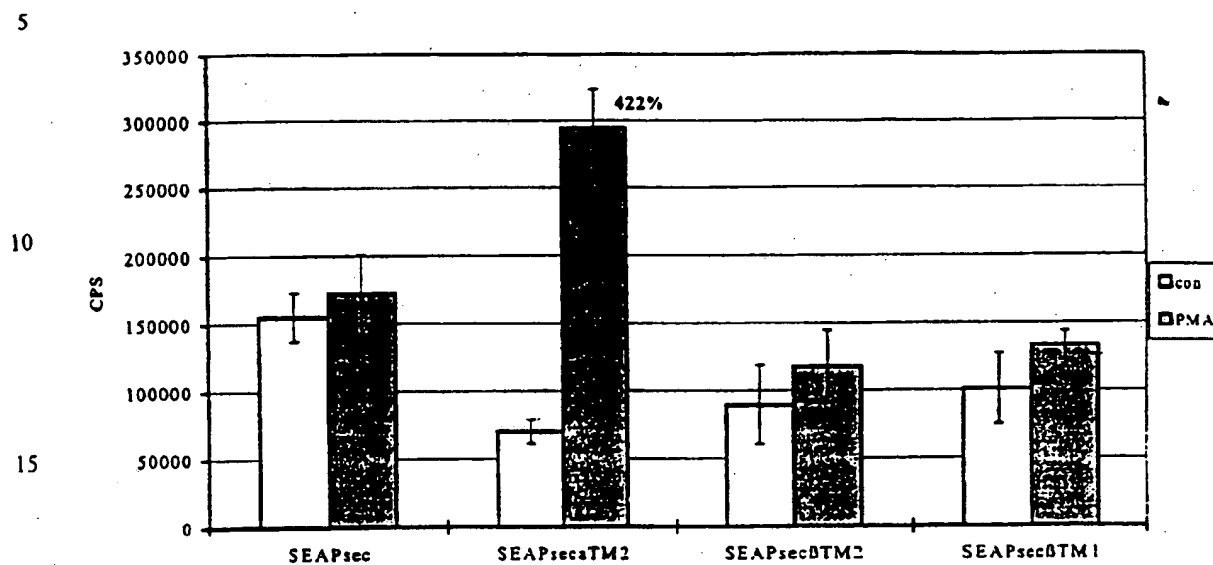
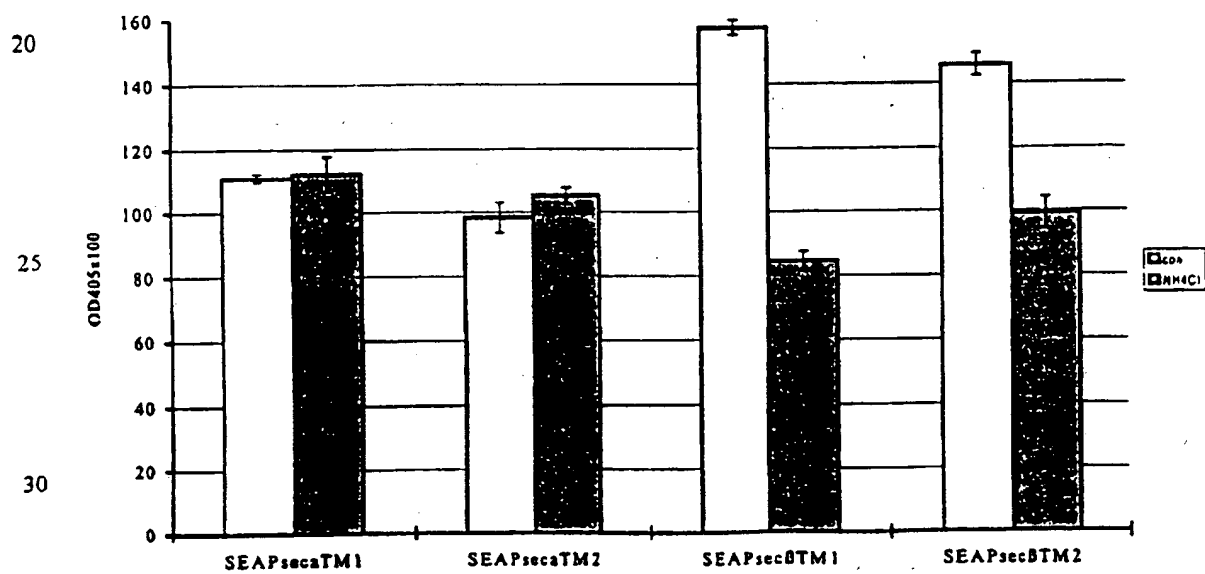


Fig. 3

A)



B)



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Fig. 4

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